| L Number | Hits | Search Text | DB | Time stamp |
|---|---|---|---|---|
| 1 | 72993 | likelihood | USPAT | 2001/12/12 07:15 |
| 2 | 143 | likelihood same allel$ | USPAT | 2001/12/12 07:15 |
| 3 | 1 | (likelihood same allel$) same forensic | USPAT | 2001/12/12 07:16 |
| 4 | 12 | (likelihood same allel$) same (probability) | USPAT | 2001/12/12 07:19 |
| 5 | 388 | likelihood adj3 ratio | USPAT | 2001/12/12 07:19 |
| 6 | 6 | (likelihood adj3 ratio) same (DNA or nucleic) | USPAT | 2001/12/12 07:19 |

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|---|---|---|
| NEWS 1 | | Web Page URLs for STN Seminar Schedule - N. America |
| NEWS 2 | Dec 17 | The CA Lexicon available in the CAPLUS and CA files |
| NEWS 3 | Feb 06 | Engineering Information Encompass files have new names |
| NEWS 4 | Feb 16 | TOXLINE no longer being updated |
| NEWS 5 | Apr 23 | Search Derwent WPINDEX by chemical structure |
| NEWS 6 | Apr 23 | PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA |
| NEWS 7 | May 07 | DGENE Reload |
| NEWS 8 | Jun 20 | Published patent applications (A1) are now in USPATFULL |
| NEWS 9 | JUL 13 | New SDI alert frequency now available in Derwent's DWPI and DPCI |
| NEWS 10 | Aug 23 | In-process records and more frequent updates now in MEDLINE |
| NEWS 11 | Aug 23 | PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA |
| NEWS 12 | Aug 23 | Adis Newsletters (ADISNEWS) now available on STN |
| NEWS 13 | Sep 17 | IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH |
| NEWS 14 | Oct 09 | Korean abstracts now included in Derwent World Patents Index |
| NEWS 15 | Oct 09 | Number of Derwent World Patents Index updates increased |
| NEWS 16 | Oct 15 | Calculated properties now in the REGISTRY/ZREGISTRY File |
| NEWS 17 | Oct 22 | Over 1 million reactions added to CASREACT |
| NEWS 18 | Oct 22 | DGENE GETSIM has been improved |
| NEWS 19 | Oct 29 | AAASD no longer available |
| NEWS 20 | Nov 19 | New Search Capabilities USPATFULL and USPAT2 |
| NEWS 21 | Nov 19 | TOXCENTER(SM) - new toxicology file now available on STN |
| NEWS 22 | Nov 29 | COPPERLIT now available on STN |
| NEWS 23 | Nov 29 | DWPI revisions to NTIS and US Provisional Numbers |
| NEWS 24 | Nov 30 | Files VETU and VETB to have open access |
| NEWS 25 | Dec 10 | WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002 |
| NEWS 26 | Dec 10 | DGENE BLAST Homology Search |

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|---|---|
| NEWS EXPRESS | August 15 CURRENT WINDOWS VERSION IS V6.0c, CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP), AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001 |
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FILE 'HOME' ENTERED AT 14:06:02 ON 12 DEC 2001

=> **file medline biosis caplus**

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
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=> **s guo(w)thompson**
L1 3 GUO(W) THOMPSON

=> **d 1-3 ti**

L1 ANSWER 1 OF 3 MEDLINE
Citing References
TI Tests for Hardy-Weinberg equilibrium in Japanese population.

L1 ANSWER 2 OF 3 MEDLINE
Citing References
TI The use of the STRs HUMTH01, HUMVWA31/A, HUMF13A1, HUMFES/FPS, HUMLPL in forensic application: validation studies and population data for Galicia (NW Spain).

L1 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2001 BIOSIS
Citing References
TI The use of the STRs HUMTH01, HUMVWA31/A, HUMF13A1, HUMFES/FPS, HUMLPL in forensic application: validation studies and population data for Galicia (NW Spain.

=> **d 1 bib ab**

L1 ANSWER 1 OF 3 MEDLINE
Full Text Citing References
AN 2000006511 MEDLINE
DN 20006511 PubMed ID: 10536440
TI Tests for Hardy-Weinberg equilibrium in Japanese population.
AU Katsumata Y; Mizutani M; Nozawa H; Uchihi R; Yamamoto T; Tamaki K
CS Department of Legal Medicine and Bioethics, Graduate School of Medicine, Nagoya University, Japan.
SO NIPPON HOIGAKU ZASSHI. JAPANESE JOURNAL OF LEGAL MEDICINE, (1999 Jun) 53 (2) 218-26.
Journal code: KL3; 0413715. ISSN: 0047-1887.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA Japanese
FS Priority Journals
EM 199911
ED Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991112
AB In population genetics, the absence of the departure from Hardy-Weinberg equilibrium (HWE) is usually tested when a population study of a certain DNA marker is performed to show the observed allele frequencies represent those of the whole population. The goodness-of-fit test (chi 2 test) assuming chi 2 approximation has frequently been used with classical blood type markers having a few alleles. However, new tests suitable for DNA markers having many alleles, such as homozygosity test, likelihood ratio test and **Guo-Thompson**'s (G-T') exact test, have recently been devised.

In the present study, appropriate tests for HWE was studied using population data of 206 Japanese individuals with 9 different short tandem repeat loci. Firstly, we found that the recommendation of NRC II for the treatment of rare allele frequencies (If a bin in the database contains fewer than five entries, it is pooled with adjacent bins so that no bin has fewer than five) is quite reasonable for personal identification in forensic sciences. Secondly, we proposed that homozygosity test, likelihood ratio test and G-T's exact test should be applied altogether and HWE of the sample population should be valid only when all of the three tests were cleared.

=> **d 2 bib ab**

L1 ANSWER 2 OF 3 MEDLINE

Full Text | Citing References

AN 96022707 MEDLINE
DN 96022707 PubMed ID: 7577690
TI The use of the STRs HUMTH01, HUMVWA31/A, HUMF13A1, HUMFES/FPS, HUMLPL in forensic application: validation studies and population data for Galicia (NW Spain).
AU Pestoni C; Lareu M V; Rodriguez M S; Munoz I; Barros F; Carracedo A
CS Institute of Legal Medicine, University of Santiago de Compostela, Spain.
SO INTERNATIONAL JOURNAL OF LEGAL MEDICINE, (1995) 107 (6) 283-90.
Journal code: AX1; 9101456. ISSN: 0937-9827.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199512
ED Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951207
AB The 5 tetranucleotide short tandem repeats, HUMTH01, HUMVWA31/A, HUMF13A1, HUMFES/FPS and HUMLPL were studied using different electrophoretic methods and PCR amplification conditions in order to optimize the typing conditions. A genetic population study in the population of Galicia was carried out and the allele and genotype frequencies are given. Compliance with the Hardy-Weinberg equilibrium was tested using different statistical parameters, with clear advantages resulting in favor of using the exact test (**Guo-Thompson** method) instead of conventional chi-square methods. Some statistical parameters of forensic interest (PD, CE, h) were also calculated. There were no mutations found in a total of 73 paternal meioses and 101 maternal meioses. Abnormal electrophoretic mobility was found in the AT-rich STR HUMF13A1 under non-denaturing conditions and, therefore, the use of denaturing conditions is absolutely necessary. No "stutter" bands were found, although double peaks in the HUMFES/FPS system were observed in some samples. The advantage of using automated sequencers with fluorescent technology is also reported.

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FILE 'SCISEARCH' ENTERED AT 14:07:05 ON 12 DEC 2001
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FILE COVERS 1974 TO 7 Dec 2001 (20011207/ED)

=> **s guo?/rau and 48/rvl and 1992/rpy**
42858 GUO?/RAU

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       1492370 48/RVL
       4102172 1992/RPY
L2        6042 GUO?/RAU AND 48/RVL AND 1992/RPY

=> s l2 and allel?
         65278 ALLEL?
L3         622 L2 AND ALLEL?

=> s l3 and likeli?
         33815 LIKELI?
L4          32 L3 AND LIKELI?

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5          32 DUP REM L4 (0 DUPLICATES REMOVED)

=> d 1-32 ti

L5   ANSWER 1 OF 32  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

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TI   Genetic identification of wild and domestic cats (Felis silvestris) and
     their hybrids using Bayesian clustering methods

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Citing References

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TI   An unconditional exact test for the Hardy-Weinberg equilibrium law:
     Sample-space ordering using the Bayes factor

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Citing References

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TI   Population structure of Atlantic salmon (Salmo salar L.): a range-wide
     perspective from microsatellite DNA variation

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Citing References

```
TI   Sampling genotypes in large pedigrees with loops

L5   ANSWER 5 OF 32  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

```
TI   A Bayesian approach to the identification of panmictic populations and the
     assignment of individuals

L5   ANSWER 6 OF 32  SCISEARCH  COPYRIGHT 2001 ISI (R)
```

Citing References

```
TI   Allele association studies with SSR and SNP markers at known physical
     distances within a 1 Mb region embracing the ALDH2 locus in the Japanese,
     demonstrates linkage disequilibrium extending up to 400 kb

L5   ANSWER 7 OF 32  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

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TI   Software for population genetic analyses of molecular marker data

L5   ANSWER 8 OF 32  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

TI Analysis of genotype frequencies and interlocus association for the PM, DQA1, and D1S80 loci in four populations

L5 ANSWER 9 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Mechanisms of population differentiation in marbled murrelets: Historical versus contemporary processes

L5 ANSWER 10 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI HLA polymorphism and evaluation of European, African, and Amerindian contribution to the white and mulatto populations from Parana, Brazil

L5 ANSWER 11 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Fine localization of a major disease-susceptibility locus for diffuse panbronchiolitis

L5 ANSWER 12 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI HLA class I polymorphism, as characterised by PCR-SSOP, in a Brazilian exogamic population

L5 ANSWER 13 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Validation of 15 microsatellites for parentage testing in North American bison, Bison bison and domestic cattle

L5 ANSWER 14 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Practical applications of genotypic surveys for forensic STR testing

L5 ANSWER 15 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Polymorphism of LMP2, TAP1, LMP7 and TAP2 in Brazilian Amerindians and Caucasoids: implications for the evolution of **allelic** and haplotypic diversity

L5 ANSWER 16 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Potential of microsatellites for individual assignment: the North Atlantic redfish (genus Sebastes) species complex as a case study

L5 ANSWER 17 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Definition of human interleukin-4 receptor alpha chain haplotypes and **allelic** association with atopy markers

L5 ANSWER 18 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Assessing linkage disequilibrium in a complex genetic system. I. Overall

deviation from random association

L5 ANSWER 19 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI **Allele** distribution at nine STR Loci - D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317 and D7S820 - in the Japanese population by multiplex PCR and capillary electrophoresis

L5 ANSWER 20 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Estimating European admixture in African Americans by using microsatellites and a microsatellite haplotype (CD4/Alu)

L5 ANSWER 21 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Population structure and stock identification of British Columbia coho salmon, Oncorhynchus kisutch, based on microsatellite DNA variation

L5 ANSWER 22 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Measuring departures from Hardy-Weinberg: a Markov chain Monte Carlo method for estimating the inbreeding coefficient

L5 ANSWER 23 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Microsatellite analysis of genetic population structure in an endangered salmonid: the coastal cutthroat trout (Oncorhynchus clarki clarki)

L5 ANSWER 24 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Incorporating genotypes of relatives into a test of linkage disequilibrium

L5 ANSWER 25 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI United Arab Emirates population data on three DNA tetrameric short tandem repeat loci: HUMTH01, TPOX and CSF1PO - derived using multiplex polymerase chain reaction and manual typing

L5 ANSWER 26 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI The exact test for cytonuclear disequilibria

L5 ANSWER 27 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Distribution of HLA-DQ alpha and polymarker (LDLR, GC, GYPA, HBGG, and D7S8) **alleles** in Arab and Pakistani populations living in Abu Dhabi, United Arab Emirates

L5 ANSWER 28 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Differences in Lp[a] concentrations and apo[a] polymorphs between black

and white Americans

L5 ANSWER 29 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI TESTING FOR LINKAGE DISEQUILIBRIUM IN GENOTYPIC DATA USING THE EXPECTATION-MAXIMIZATION ALGORITHM

L5 ANSWER 30 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI Statistical analysis of a large file of data from STR profiles of British Caucasians to support forensic casework

L5 ANSWER 31 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI INVESTIGATION OF THE INHERITANCE OF BIRTH-DEFECTS IN SWINE BY COMPLEX SEGREGATION ANALYSIS

L5 ANSWER 32 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Citing References

TI AN E-M ALGORITHM AND TESTING STRATEGY FOR MULTIPLE-LOCUS HAPLOTYPES

=> **d 5, 6 bib ab**

L5 ANSWER 5 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Full Text | Citing References

AN 2001:707762 SCISEARCH
GA The Genuine Article (R) Number: 468CV
TI A Bayesian approach to the identification of panmictic populations and the assignment of individuals
AU Dawson K J (Reprint); Belkhir K
CS Univ Montpellier 2, Lab Genome Populat & Interact, CNRS, UMR 5000, Pl Eugene Bataillon, F-34095 Montpellier 5, France (Reprint); Univ Montpellier 2, Lab Genome Populat & Interact, CNRS, UMR 5000, F-34095 Montpellier 5, France; Univ Bristol, Dept Agr Sci, IACR, Long Ashton Res Stn, Bristol BS41 9AF, Avon, England
CYA France; England
SO GENETICAL RESEARCH, (AUG 2001) Vol. 78, No. 1, pp. 59-77.
Publisher: CAMBRIDGE UNIV PRESS, 110 MIDLAND AVE, PORT CHESTER, NY 10573-9863 USA.
ISSN: 0016-6723.
DT Article; Journal
LA English
REC Reference Count: 44
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB We present **likelihood**-based methods for assigning the individuals in a sample to source populations, on the basis of their genotypes at co-dominant marker loci. The source populations are assumed to be at Hardy-Weinberg and linkage equilibrium, but the **allelic** composition of these source populations and even the number of source populations represented in the sample are treated as uncertain. The parameter of interest is the partition of the set of sampled individuals, induced by the assignment of individuals to source populations. We present a maximum **likelihood** method, and then a more powerful Bayesian approach for estimating this sample partition. In general, it will not be feasible to evaluate the evidence supporting each possible partition of the sample. Furthermore, when the number of individuals in the sample is large, it may not even be feasible to evaluate the evidence supporting, individually,

each of the most plausible partitions because there may be many individuals which are difficult to assign. To overcome these problems, we use low-dimensional marginals (the 'co-assignment probabilities') of the posterior distribution of the sample partition as measures of 'similarity', and then apply a hierarchical clustering algorithm to identify clusters of individuals whose assignment together is well supported by the posterior distribution, A binary tree provides a visual representation of how well the posterior distribution supports each cluster in the hierarchy. These methods are applicable to other problems where the parameter of interest is a partition of a set. Because the co-assignment probabilities are independent of the arbitrary labelling of source populations, we avoid the label-switching problem of previous Bayesian methods.

L5 ANSWER 6 OF 32 SCISEARCH COPYRIGHT 2001 ISI (R)

Full Text | Citing References

AN 2001:18014 SCISEARCH
GA The Genuine Article (R) Number: 384UY
TI **Allele** association studies with SSR and SNP markers at known physical distances within a 1 Mb region embracing the ALDH2 locus in the Japanese, demonstrates linkage disequilibrium extending up to 400 kb
AU Koch H G; McClay J; Loh E W; Higuchi S; Zhao J H; Sham P; Ball D; Craig I W (Reprint)
CS Inst Psychiat, SGDP Res Ctr, Denmark Hill, London SE5 8AF, England (Reprint); Inst Psychiat, SGDP Res Ctr, London SE5 8AF, England; Kurihama Natl Hosp, Kanagawa, Japan
CYA England; Japan
SO HUMAN MOLECULAR GENETICS, (12 DEC 2000) Vol. 9, No. 20, pp. 2993-2999. Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND. ISSN: 0964-6906.
DT Article; Journal
LA English
REC Reference Count: 40
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB There has been considerable recent debate concerning the distances over which revels of **allelic** association useful for genomic quantitative trait locus (QTL) scans can be detected. We have examined simple sequence repeat (SSR) polymorphisms and two single nucleotide polymorphisms (SNPs) in the region flanking the aldehyde dehydrogenase 2 locus, ALDH2, in populations of Japanese alcoholics and controls. These groups differ significantly in the **allele** frequencies for the functional SNP in exon XII of this gene located on chromosome 12. The results obtained with SSR markers complement recent investigations with SNPs over similar distances at the TCR alpha/delta locus. Significant **allelic** association with this marker could be detected for SSRs over distances up to 400 kb and over 37 kb for the SNP thereby extending the distance over which LD at this locus could be detected by an order of magnitude. Furthermore, as a proof of principle, we show that comparisons of **allele** frequency differences for the SSR markers in the case (alcoholics) and control populations would have detected the ALDH2 marker as a putative QTL. Extending the tests to include **alleles** at two or three flanking loci suggests that the power to detect QTLs through association can be enhanced significantly.

=> **d his**

(FILE 'HOME' ENTERED AT 14:06:02 ON 12 DEC 2001)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:06:14 ON 12 DEC 2001
L1 3 S GUO(W)THOMPSON

FILE 'SCISEARCH' ENTERED AT 14:07:05 ON 12 DEC 2001
L2 6042 S GUO?/RAU AND 48/RVL AND 1992/RPY

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L3          622 S L2 AND ALLEL?
L4           32 S L3 AND LIKELI?
L5           32 DUP REM L4 (0 DUPLICATES REMOVED)

=> s l3 and proceedings?/jt
        177712 PROCEEDINGS?/JT
                  (PROCEEDINGS?/JT)
L6           4 L3 AND PROCEEDINGS?/JT

=> d 1-4 ti

L6   ANSWER 1 OF 4  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

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TI   Genetic consequences of population decline in the European otter (Lutra
     lutra): an assessment of microsatellite DNA variation in Danish otters
     from 1883 to 1993

L6   ANSWER 2 OF 4  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

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TI   Major histocompatibility complex variation associated with juvenile
     survival and parasite resistance in a large unmanaged ungulate population
     (Ovis aries L.)

L6   ANSWER 3 OF 4  SCISEARCH  COPYRIGHT 2001 ISI (R)
```

Citing References

```
TI   ALLELIC ASSOCIATIONS OF 2 POLYMORPHIC MICROSATELLITES IN INTRON-40 OF
     THE HUMAN VON-WILLEBRAND-FACTOR GENE

L6   ANSWER 4 OF 4  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Citing References

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TI   POPULATION-GENETICS IN THE FORENSIC DNA DEBATE


=> d 2-4 bib ab

L6   ANSWER 2 OF 4  SCISEARCH  COPYRIGHT 2001 ISI (R)
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Full Text | Citing References

```
AN   1998:275881  SCISEARCH
GA   The Genuine Article (R) Number: ZE957
TI   Major histocompatibility complex variation associated with juvenile
     survival and parasite resistance in a large unmanaged ungulate population
     (Ovis aries L.)
AU   Paterson S; Wilson K; Pemberton J M (Reprint)
CS   UNIV EDINBURGH, INST CELL ANIM & POPULAT BIOL, W MAINS RD, EDINBURGH EH9
     3JT, MIDLOTHIAN, SCOTLAND (Reprint); UNIV EDINBURGH, INST CELL ANIM &
     POPULAT BIOL, EDINBURGH EH9 3JT, MIDLOTHIAN, SCOTLAND; UNIV CAMBRIDGE,
     DEPT GENET, CAMBRIDGE CB2 3EH, ENGLAND; UNIV STIRLING, DEPT BIOL & MOL
     SCI, STIRLING FK9 4LA, SCOTLAND
CYA  SCOTLAND; ENGLAND
SO   PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
     AMERICA, (31 MAR 1998) Vol. 95, No. 7, pp. 3714-3719.
     Publisher: NATL ACAD SCIENCES, 2101 CONSTITUTION AVE NW, WASHINGTON, DC
     20418.
     ISSN: 0027-8424.
DT   Article; Journal
FS   LIFE
LA   English
REC  Reference Count: 55
```

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB Antagonistic coevolution between hosts and parasites has been proposed as a mechanism maintaining genetic diversity in both host and parasite populations, In particular, the high levels of genetic diversity widely observed at the major histocompatibility complex (MHC) of vertebrate hosts are consistent with the hypothesis of parasite-driven balancing selection acting to maintain MHC genetic diversity, To date, however, empirical evidence in support of this hypothesis, especially from natural populations, has been lacking, A large unmanaged population of Soay sheep (Ovis aries L.) is used to investigate associations between MHC variation, juvenile survival, and parasite resistance. We show in an unmanaged, nonhuman population that **allelic** variation within the MHC is significantly associated with differences in both juvenile survival and resistance to intestinal nematodes, Certain MHC **alleles** are associated with low survivorship probabilities and high levels of parasitism or vies versa, We conclude that parasites ape likely to play a major role in the maintenance of MHC diversity In this population.

L6 ANSWER 3 OF 4 SCISEARCH COPYRIGHT 2001 ISI (R)

Full Text | Citing References

AN 94:47939 SCISEARCH
GA The Genuine Article (R) Number: MR989
TI **ALLELIC** ASSOCIATIONS OF 2 POLYMORPHIC MICROSATELLITES IN INTRON-40 OF THE HUMAN VON-WILLEBRAND-FACTOR GENE
AU PENA S D J (Reprint); DESOUZA K T; DEANDRADE M; CHAKRABORTY R
CS NUCLEO GENET MED MINAS GERAIS GENE MG, BR-30130909 BELO HORIZONTE, MG, BRAZIL (Reprint); UNIV FED MINAS GERAIS, DEPT BIOCHEM, BR-30161970 BELO HORIZONTE, MG, BRAZIL; UNIV TEXAS, GRAD SCH BIOMED SCI, CTR DEMOG & POPULAT GENET, HOUSTON, TX, 77225
CYA BRAZIL; USA
SO **PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA**, (18 JAN 1994) Vol. 91, No. 2, pp. 723-727.
ISSN: 0027-8424.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 33

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB At intron 40 of the von Willebrand factor (vWF) gene, two GATA-repeat polymorphic sites exist that are physically separated by 212 bp. At the first site (vWF1 locus), seven segregating repeat:**alleles** were observed in a Brazilian Caucasian population, and at the second (vWFZ locus) there were eight **alleles**, detected through PCR amplifications of this DNA region. Haplotype analysis of individuals revealed 36 different haplotypes in a sample of 338 chromosomes examined. **Allele** frequencies between generations and gender at each locus were not significantly different, and the genotype frequencies were consistent with their Hardy-Weinberg expectations. Linkage disequilibrium between loci is highly significant with positive **allele** size association; that is, large **alleles** at the loci tend to occur together, and so do the small **alleles**. Variability at each locus appeared to have arisen in a stepwise fashion, suggesting replication slippage as a possible mechanism of production of new **alleles**. However, we observed an increased number of haplotypes, in contrast with the predictions of a stepwise production of variation in the entire region, suggesting some form of ''cooperative'' changes between loci that could be due to either gene conversion, or a common control mechanism of production of new variation at these repeat polymorphism sites. The high degree of polymorphism (gene diversity values of 72% and 78% at vWF1 and vWFZ, respectively, and of 93% at the haplotype level) makes these markers informative for paternity testing, genetic counseling, and individual-identification purposes.

L6 ANSWER 4 OF 4 SCISEARCH COPYRIGHT 2001 ISI (R)

Full Text | Citing References

AN 92:735562 SCISEARCH
GA The Genuine Article (R) Number: KC844
TI POPULATION-GENETICS IN THE FORENSIC DNA DEBATE
AU WEIR B S (Reprint)
CS N CAROLINA STATE UNIV, DEPT STAT, PROGRAM STAT GENET, RALEIGH, NC, 27695 (Reprint)
CYA USA
SO **PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA**, (15 DEC 1992) Vol. 89, No. 24, pp. 11654-11659.
ISSN: 0027-8424.
DT General Review; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 64
*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB The use of matching variable number of tandem repeat (VNTR) profiles to link suspects with crimes is potentially very powerful, but it has been quite controversial. Initial debate over laboratory procedures has largely given way to debate over the statistical and population genetic issues involved in calculating the frequency of a profile for a random member of a population. This frequency is used to weight the evidence of a match between suspect and crime scene material when the suspect denies responsibility for that material. A recent report from the National Research Council, intended to put to rest some of the issues, has instead raised further debate by advocating a procedure based on maximum frequencies of profile components over several different populations.

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| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|---|---|---|
| FULL ESTIMATED COST | 29.12 | 34.38 |

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=> **s guo (2a) thompson**
L7 8 GUO (2A) THOMPSON

=> **d his**

(FILE 'HOME' ENTERED AT 14:06:02 ON 12 DEC 2001)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:06:14 ON 12 DEC 2001
L1 3 S GUO(W)THOMPSON

FILE 'SCISEARCH' ENTERED AT 14:07:05 ON 12 DEC 2001
L2 6042 S GUO?/RAU AND 48/RVL AND 1992/RPY
L3 622 S L2 AND ALLEL?
L4 32 S L3 AND LIKELI?
L5 32 DUP REM L4 (0 DUPLICATES REMOVED)
L6 4 S L3 AND PROCEEDINGS?/JT

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:12:19 ON 12 DEC 2001
L7 8 S GUO (2A) THOMPSON

=> **s l7 not l1**
L8 5 L7 NOT L1

=> **dup rem l8**
PROCESSING COMPLETED FOR L8
L9 3 DUP REM L8 (2 DUPLICATES REMOVED)

=> **d 1-3 bib ab**

L9 ANSWER 1 OF 3 MEDLINE DUPLICATE 1
Full Text | Citing References

AN 1999153468 MEDLINE
DN 99153468 PubMed ID: 10030397
TI Computing probabilities of homozygosity by descent.
AU Schaffer A A
CS National Human Genome Research Institute, National Institutes of Health, Bethesda, Maryland, USA.. schaffer@nhgri.nih.gov
SO GENETIC EPIDEMIOLOGY, (1999) 16 (2) 135-49.
Journal code: FMP; 8411723. ISSN: 0741-0395.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199904
ED Entered STN: 19990420
Last Updated on STN: 19990420
Entered Medline: 19990407
AB A person is autozygous at a locus if the person inherits the same allele twice identical by descent along two distinct paths from the same ancestor. Autozygosity is a common cause of recessive diseases in inbred populations. Homozygosity mapping uses this fact to locate the genes that cause recessive diseases. The probability of autozygosity can be used to estimate the probability of a true positive and of a false positive in homozygosity mapping. **Thompson** [1994] and **Guo** [1997] therefore studied the problem of computing the prior, unconditional (multilocus) probability of autozygosity (MPA). I consider a different quantity: the interval probability of autozygosity (IPA). The two measures are identical in the single-locus case. IPA has two notable advantages over MPA: 1. IPA does not include the possibility of heterozygous regions between the homozygous markers. 2. IPA can be computed in time that is polynomial in the pedigree size. My polynomial-time algorithm for the single-locus case solves a problem mentioned by Guo. I implemented a program to compute the IPA. The contribution of this work is the application of basic, abstract methods from computer science to address a problem in genetics.

L9 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS
Full Text | Citing References

AN 1998:139400 CAPLUS
TI Semiclassical calculations of tunneling in aziridine.
AU Wilson, A. K.; Guo, Y.; Chabalowski, C. F.; Thompson, D. L.
CS Department Chemistry, Oklahoma State University, Stillwater, OK, 74078, USA
SO Book of Abstracts, 215th ACS National Meeting, Dallas, March 29-April 2 (1998), COMP-204 Publisher: American Chemical Society, Washington, D. C.
CODEN: 65QTAA
DT Conference; Meeting Abstract
LA English
AB We have performed ab initio MP2 calcns. to det. the equil. and transition state structures and vibrational spectra for aziridine. These results were used to construct an analytic potential energy surface. Full-dimensional semi-classical calcns. [Sewell, **Guo**, and **Thompson**, J.

Chem. Phys. 103, 8557 (1995)] using this potential have been carried out for the proton tunneling between the wells of the two aziridine isomers.

L9 ANSWER 3 OF 3 MEDLINE DUPLICATE 2

Full Text | Citing References

AN 93035376 MEDLINE
DN 93035376 PubMed ID: 1415253
TI A Monte Carlo method for combined segregation and linkage analysis.
AU Guo S W; Thompson E A
CS Department of Biostatistics, University of Michigan, Ann Arbor.
NC GM-46255 (NIGMS)
HL30086 (NHLBI)
P30-HG00209 (NHGRI)
SO AMERICAN JOURNAL OF HUMAN GENETICS, (1992 Nov) 51 (5) 1111-26.
Journal code: 3IM; 0370475. ISSN: 0002-9297.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199211
ED Entered STN: 19930122
Last Updated on STN: 19980206
Entered Medline: 19921112
AB We introduce a Monte Carlo approach to combined segregation and linkage analysis of a quantitative trait observed in an extended pedigree. In conjunction with the Monte Carlo method of likelihood-ratio evaluation proposed by **Thompson** and **Guo**, the method provides for estimation and hypothesis testing. The greatest attraction of this approach is its ability to handle complex genetic models and large pedigrees. Two examples illustrate the practicality of the method. One is of simulated data on a large pedigree; the other is a reanalysis of published data previously analyzed by other methods.

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